

<!--StartFragment-->RESULT 1

AAW10593

ID AAW10593 standard; protein; 257 AA.

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AC AAW10593;

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DT 15-JUN-2007 (revised)

DT 29-OCT-1997 (first entry)

XX

DE Hevea brasiliensis S-hydroxynitrilase.

XX

KW S-hydroxynitrilase; chiral synthesis; aliphatic; aromatic; S-cyanohydrin;  
KW recombinant; BOND\_PC; hydroxynitrile lyase; G016829; G046991; G08152.

XX

OS Hevea brasiliensis.

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PN W09703204-A2.

XX

PD 30-JAN-1997.

XX

PF 10-JUL-1996; 96WO-EP003010.

XX

PR 12-JUL-1995; 95AT-00001182.

XX

PA (STAM ) DSM CHEMIE LINZ GMBH.

XX

PI Hasslacher M, Schall M, Schwab H, Hayn EM, Kohlwein S, Griengl H;

XX

DR WPI; 1997-119058/11.

DR N-PSDB; AAT36351.

DR PC:NCBI; gi1708278.

DR PC:SWISSPROT; P52704.

DR PC:BIND; 229823,256092,229822,256091,74321.

XX

PT Hevea brasiliensis S-hydroxy:nitrilase - and recombinant equivalent of  
PT high specific activity, for chiral synthesis of cyano:hydrin(s).

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PS Claim 2; Page 2-3; 14pp; German.

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CC The present sequence is the Hevea brasiliensis S-hydroxynitrilase (S-HN),  
CC which can be used for the chiral synthesis of aliphatic or aromatic S-  
CC cyanohydrins from HCN, or its donor, and ketone. Recombinant S-HN has  
CC higher specific activity than the native enzyme. H. brasiliensis leaves  
CC were homogenised in cold pH 6.5 K phosphate buffer, and the extract  
CC subjected to sequential chromatography on QAE-Sepharose, Phenyl-Sepharose  
CC and BioGel 150 to recover a protein with a specific activity of 19 IU/mg.  
CC A cDNA library was prepared from young H. brasiliensis leaves in Zap  
CC phase, and screened with polyclonal rabbit antiserum raised against the  
CC purified enzyme. The insert in one positive clone was isolated, and

CC ligated into pBluescript to form pHNL-100. This plasmid, in E. coli SOLR,  
 CC expressed a fusion protein with lacZ that was immunoreactive. Sequencing  
 CC showed that the insert in this plasmid was not complete, and the missing  
 CC 5'-end generated by 2 stage PCR, resulting in plasmid pHNL-101,  
 CC containing the entire coding sequence

CC

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed  
 CC information from BOND.

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SQ Sequence 257 AA;

Query Match 100.0%; Score 1370; DB 2; Length 257;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-138;  
 Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFAHFVLIHTICHGAWIWHKLKPLLEALGHKVTALDLAASGVDPRIIEIGSFDEYSEP 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 MAFAHFVLIHTICHGAWIWHKLKPLLEALGHKVTALDLAASGVDPRIIEIGSFDEYSEP 60

Qy 61 LLTFLEALPPGEKVILVGESCGGLNIAIAADKYCEKIAAAVFHNSVLPDTEHCPSYVVDK 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 LLTFLEALPPGEKVILVGESCGGLNIAIAADKYCEKIAAAVFHNSVLPDTEHCPSYVVDK 120

Qy 121 LMEVFPDWKDTTYFTYTKDGKEITGLKLGFTLLRENLYTLCGP EYE LAKMLTRKGS LFQ 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 LMEVFPDWKDTTYFTYTKDGKEITGLKLGFTLLRENLYTLCGP EYE LAKMLTRKGS LFQ 180

Qy 181 NILAKRPFFTKEGYGSIKKIYVWTDQDEIFLPEFQLWQIENYKPDKVYKVEGGDHKLQLT 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 NILAKRPFFTKEGYGSIKKIYVWTDQDEIFLPEFQLWQIENYKPDKVYKVEGGDHKLQLT 240

Qy 241 KTKEIAEILQE VADTYN 257  
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 Db 241 KTKEIAEILQE VADTYN 257  
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